

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

This listing of claims will replace all prior versions and listings of claims in the application:

1. (Previously Presented) A primer which amplifies *groEL2* gene fragment of at least one *Streptomyces* species consisting of the nucleotide sequence of SEQ ID NO: 1.

2. (Previously Presented) A primer which amplifies *groEL2* gene fragment of at least one *Streptomyces* species consisting of the nucleotide sequence of SEQ ID NO: 2.

3. (Withdrawn) A *groEL2* gene fragment derived from *Streptomyces* species or fragment thereof comprising a polynucleotide chosen from the nucleotide sequences of SEQ ID NOs: 3 to 42.

4. (Previously Presented) An isolated *groEL2* gene fragment from *S. scabiei* comprising SEQ ID NO: 43.

5. (Withdrawn-Currently Amended) A method for identifying at least one *Streptomyces* species comprising:

a) amplifying *groEL2* gene fragment of target strain microorganism using a the primer according to claim 1 or 2 ~~which is capable of specifically amplifying *groEL2* gene of *Streptomyces* species;~~

b) analyzing the nucleotide sequence of *groEL2* gene fragment thus amplified;
and

c) comparing the nucleotide sequence obtained in b) with that of *groEL2* gene fragment of a reference strain microorganism.

6. (Withdrawn-Currently Amended) The method of claim 5, wherein the microorganism is chosen from *R. equi*, *S. acrimycini*, *S. aculeolatus*, *S. alanosinicus*, *S. albireticuli*, *S. albofaciens*, *S. albogriseolus*, *S. alboniger*, *S. albus*, *S. ambofaciens*, *S. aminophilus*, *S. anandii*, *S. argenteolus*, *S. bambergiensis*, *S. capillispiralis*, *S. carpinesis*, *S. catenulae*, *S. cellulosa*, *S. chartreusis*, *S. chattanoogensis*, *S. cinereoruber*, *S. cinnamomensis*, *S. cirratus*, *S. coeruleorubidus*, *S. collinus*, *S. corchorusii*, *S. diastaticus*, *S. djakartensis*, *S. erumpens*, *S. fulvissimus*, *S. galilaeus*, *S. griseochromogenes*, *S. griseolus*, *S. griseoviridis*, *S. humiferus*, *S. hygrosopicus*, *S. minutiscleroticus*, *S. murinus*, *S. nodosus*, *T. paurometabola*, *S. acidiscabies*, *S. bottropensis*, *S. disastatochromogenes*, *S. neyagawaensis*, *S. scabiei*, and *S. turgidiscabies* primer is chosen from at least one of

a) ~~a primer comprising the nucleotide sequence of SEQ ID NO: 1 and~~

b) ~~a primer comprising the nucleotide sequence of SEQ ID NO: 2.~~

7. (Withdrawn-Currently Amended) The method of claim 5, wherein the *groEL2* gene fragment of a reference strain microorganism is chosen from the nucleotide sequences of SEQ ID NOs: 3 to 42.

8. (Withdrawn-Currently Amended) The method of claim 5, wherein the *groEL2* gene fragment of a reference strain microorganism is chosen from the nucleotide sequences of SEQ ID NOs: 43 to 61.

9. (Withdrawn) The method of claim 5, wherein c) further comprises multi-aligning the nucleotide sequences and forming a phylogenetic tree.

10. (Currently Amended) A primer which specifically amplifies *groEL2* gene fragment of ~~at least one~~ *Streptomyces* species consisting ~~essentially~~ of the nucleotide sequence of SEQ ID NO: 2.

11. (Cancelled)

12. (Previously Presented) The *groEL2* gene fragment of claim 4, wherein the fragment is SEQ ID NO: 43.

13. (Withdrawn) An isolated *groEL2* gene fragment derived from a potato scab pathogenic microorganism comprising a polynucleotide chosen from the nucleotide sequences of any one of SEQ ID NOs: 44 to 61.

14. (Currently Amended) An isolated *groEL2* gene fragment produced by amplification from a microorganism using

a) a primer consisting of the nucleotide sequence of SEQ ID NO: 1 and

b) a primer consisting of the nucleotide sequence of SEQ ID NO: 2,

wherein said microorganism is chosen from *R. equi*, *S. acrimycini*,
S. aculeolatus, *S. alanosinicus*, *S. albireticuli*, *S. albofaciens*, *S. albogriseolus*,
S. alboniger, *S. albus*, *S. ambofaciens*, *S. aminophilus*, *S. anandii*, *S. argenteolus*,
S. bambergensis, *S. capillispiralis*, *S. carpinesis*, *S. catenulae*, *S. cellulosa*,
S. chartreusis, *S. chattanoogensis*, *S. cinereoruber*, *S. cinnamonensis*, *S. cirratus*,
S. coeruleorubidus, *S. collinus*, *S. corchorusii*, *S. diastaticus*, *S. djakartensis*,
S. erumpens, *S. fulvissimus*, *S. galilaeus*, *S. griseochromogenes*, *S. griseolus*,

S. griseoviridis, *S. humiferus*, *S. hygroscopicus*, ~~*S. hygroscopicus*~~, *S. minutiscleroticus*,
S. murinus, *S. nodosus*, *T. paurometabola*, *S. acidiscabies*, *S. bottropensis*,
S. disastatochromogenes, *S. neyagawaensis*, *S. scabiei*, and *S. turgidiscabies*.